

What is claimed is:

1. An isolated polypeptide, comprising an amino acid sequence selected from SEQ ID NOS: 14, 16, 18, 20, 22 and 24.
- 5           2. An isolated polypeptide, comprising
  - a) an amino acid sequence having at least 50% amino acid identity with SEQ ID NO: 10, and
  - b) an amino acid sequence selected from SEQ ID NOS: 14, 16, 18, 20, 22, and 24; or a conservative  
10 variant thereof.
3. An isolated polypeptide, comprising an amino acid sequence selected from SEQ ID NOS: 2, 4, 6 and 8.
- 15           4. An isolated polypeptide, consisting of an amino acid sequence selected from SEQ ID NOS: 2, 4, 6 and 8.
5. A COX-1 variant binding agent, which binds an amino acid sequence selected from SEQ ID NOS: 14, 16 and 18; or an epitope thereof.
- 20           6. The binding agent of claim 5, wherein said binding agent is an antibody, or antigen binding fragment thereof.
7. A cell, comprising the exogenously expressed polypeptide of claim 1, 2, or 3.

8. A method for identifying a compound that modulates a COX-1 variant, comprising:

a) contacting said COX-1 variant with a compound, wherein said COX-1 variant is an isolated COX-1 variant or a COX-1 variant over-expressed in a genetically engineered cell, and

b) determining the level of an indicator, which correlates with modulation of a COX-1 variant, wherein an alteration in the level of said indicator as compared to a control level indicates that said compound is a compound that modulates a COX-1 variant.

9. The method of claim 8, wherein said alteration is an increase in the level of said indicator.

10. The method of claim 8, wherein said alteration is a decrease in the level of said indicator.

11. The method of claim 8, wherein said COX-1 variant in step (a) is the polypeptide of claim 2.

12. The method of claim 8, wherein said COX-1 variant in step (a) is the polypeptide of claim 3.

13. The method of claim 8, wherein said COX-1 variant in step (a) is an isolated COX-1 variant polypeptide.

14. The method of claim 8, wherein said COX-1 variant in step (a) is a COX-1 variant over-expressed in a genetically engineered cell.

15. The method of claim 14, wherein said COX-1 variant is exogenously expressed.

16. The method of claim 8, wherein said indicator is prostaglandin E<sub>2</sub> (PGE<sub>2</sub>).

5 17. The method of claim 8, wherein said compound is a small molecule.

18. The method of claim 8, wherein said compound is a polypeptide.

19. A method for identifying a compound that  
10 specifically binds to a COX-1 variant, comprising:

a) contacting said COX-1 variant with a compound, wherein said COX-1 variant is an isolated COX-1 variant or a COX-1 variant over-expressed in a genetically engineered cell, and

15 b) determining specific binding of said compound to said COX-1 variant.

20. The method of claim 19, wherein said COX-1 variant in step (a) is the polypeptide of claim 2.

21. The method of claim 19, wherein said COX-1  
20 variant in step (a) is the polypeptide of claim 3.

22. The method of claim 19, wherein said COX-1 variant in step (a) is an isolated COX-1 polypeptide.

23. The method of claim 19, wherein said COX-1 in step (a) is a COX-1 variant over-expressed in a  
25 genetically engineered cell.

24. The method of claim 23, wherein said COX-1 variant is exogenously expressed.

25. The method of claim 19, wherein said contacting occurs *in vitro*.

5           26. The method of claim 19, wherein said compound is a small molecule.

27. The method of claim 19, wherein said compound is a polypeptide.

28. A method for identifying a compound that differentially modulates a COX-1 variant, comprising:

a) contacting said COX-1 variant with a compound, wherein said COX-1 variant is an isolated COX-1 variant or a COX-1 variant over-expressed in a genetically engineered cell;

b) determining the level of an indicator which correlates with modulation of said COX-1 variant;

c) contacting a second COX enzyme with said compound;

d) determining the level of a corresponding indicator which correlates with modulation of said second COX enzyme; and

e) comparing the level of the indicator from step (b) with the level of the corresponding indicator from step (d), wherein a different level of the indicator from step (b) compared to the level of the corresponding indicator from step (d) indicates that said compound is a compound that differentially modulates said COX-1 variant.

29. The method of claim 28, wherein said second COX enzyme is a different COX-1 variant.

30. The method of claim 28, wherein said second COX enzyme comprises the amino acid sequence SEQ ID NO: 10, or a functional fragment thereof.

31. The method of claim 28, wherein said second COX enzyme comprises the amino acid sequence SEQ ID NO: 26, or a functional fragment thereof.

32. The method of claim 28, wherein the level  
5 of said indicator from step (b) is greater than the level of said corresponding indicator from step (d).

33. The method of claim 28, wherein the level of said indicator from step (b) is less than the level of said corresponding indicator from step (d).

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34. The method of claim 28, wherein said COX-1 variant in step (a) is the polypeptide of claim 2.

35. The method of claim 28, wherein said COX-1 variant in step (a) is the polypeptide of claim 3.

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36. The method of claim 28, wherein said COX-1 variant in step (a) is an isolated COX-1 polypeptide.

37. The method of claim 28, wherein said COX-1 variant in step (a) is a COX-1 variant over-expressed in a genetically engineered cell.

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38. The method of claim 37, wherein said COX-1 variant is exogenously expressed.

39. The method of claim 28, wherein said indicator in step (b) is prostaglandin E<sub>2</sub> (PGE<sub>2</sub>).

40. The method of claim 28, wherein said  
25 compound is a small molecule.

41. The method of claim 28, wherein said compound is a polypeptide.

42. A method for identifying a compound that differentially binds to a COX-1 variant, comprising:

5           a) contacting said COX-1 variant with a compound, wherein said COX-1 variant is an isolated COX-1 or a COX-1 variant over-expressed in a genetically engineered cell;

          b) determining specific binding of said  
10 compound to said COX-1 variant;

          c) contacting a second COX enzyme with said compound;

          d) determining specific binding of said compound to said second COX enzyme; and

15           e) comparing the level of specific binding from step (b) with the level of specific binding from step (d), wherein a different level of specific binding from step (b) compared to the level of specific binding from step (d) indicates that said compound is a compound that  
20 differentially binds to a COX-1 variant.

43. The method of claim 42, wherein said second COX enzyme is a different COX-1 variant.

44. The method of claim 42, wherein said second COX enzyme comprises the amino acid sequence SEQ  
25 ID NO: 10, or a functional fragment thereof.

45. The method of claim 42, wherein said second COX enzyme comprises the amino acid sequence SEQ ID NO: 26, or a functional fragment thereof.

46. The method of claim 42, wherein said  
5 different level of specific binding is an increased level of binding.

47. The method of claim 42, wherein said different level of specific binding is a decreased level of binding.

10 48. The method of claim 42, wherein said COX-1 variant in step (a) is the polypeptide of claim 2.

49. The method of claim 42, wherein said COX-1 variant in step (a) is the polypeptide of claim 3.

15 50. The method of claim 42, wherein said COX-1 variant in step (a) is an isolated COX-1 polypeptide.

51. The method of claim 42, wherein said COX-1 variant in step (a) is a COX-1 variant over-expressed in a genetically engineered cell.

20 52. The method of claim 51, wherein said COX-1 variant is exogenously expressed.

53. The method of claim 42, wherein said contacting occurs *in vitro*.

54. The method of claim 42, wherein said compound is a small molecule.



55. The method of claim 42, wherein said compound is a polypeptide.

56. An isolated nucleic acid molecule,  
comprising a nucleotide sequence that encodes a  
5 polypeptide comprising

a) an amino acid sequence having at least 50% amino acid identity with SEQ ID NO: 10, and

b) an amino acid sequence selected from SEQ ID NOS: 20, 22 and 24; or a conservative variant thereof.

10 57. An isolated nucleic acid molecule,  
comprising a nucleotide sequence that encodes an amino acid sequence selected from SEQ ID NOS: 2, 4, 6 and 8.

58. An isolated nucleic acid molecule,  
consisting of a nucleotide sequence selected from SEQ ID  
15 NOS: 1, 3, 5 and 7.

59. A vector, comprising the isolated nucleic acid molecule as in claims 56, 57 or 58.

60. A host cell, comprising the vector of  
20 claim 59.